

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,261A

DATE: 10/03/2001
TIME: 08:45:06

Input Set : A:\Hj5001us.app
Output Set: N:\CRF3\10032001\I762261A.raw

3 <110> APPLICANT: Quinnan, Gerald V.
 4 Zhang, Peng Fei
 6 <120> TITLE OF INVENTION: Expression and Characterization of HIV-1 Envelope
 7 Protein Associated with a Broadly Reactive Neutralizing
 8 Antibody Response
 10 <130> FILE REFERENCE: 44508-5001-US
 12 <140> CURRENT APPLICATION NUMBER: US 09/762,261A
 13 <141> CURRENT FILING DATE: 2001-02-05
 15 <150> PRIOR APPLICATION NUMBER: US 60/095,267
 16 <151> PRIOR FILING DATE: 1998-08-04
 18 <150> PRIOR APPLICATION NUMBER: PCT/US99/17596
 19 <151> PRIOR FILING DATE: 1999-08-04
 21 <160> NUMBER OF SEQ ID NOS: 4
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 866
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Human immunodeficiency virus type 1
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: R2 strain envelope protein (gp 160)
 33 <400> SEQUENCE: 1
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 37 Gly Thr Met Leu Leu Gly Leu Leu Met Ile Cys Ser Ala Thr Glu Lys
 38 20 25 30
 40 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
 41 35 40 45
 43 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ala
 44 50 55 60
 46 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 47 65 70 75 80
 49 Gln Glu Val Glu Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp Lys
 50 85 90 95
 52 Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
 53 100 105 110
 55 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
 56 115 120 125
 58 Asn Cys Thr Asp Leu Arg Asn Thr Thr Asn Thr Asn Asn Ser Thr Asp
 59 130 135 140
 61 Asn Asn Asn Ser Asn Ser Glu Gly Thr Ile Lys Gly Gly Glu Met Lys
 62 145 150 155 160
 64 Asn Cys Ser Phe Asn Ile Ala Thr Ser Ile Gly Asp Lys Met Gln Lys
 65 165 170 175
 67 Glu Tyr Ala Leu Leu Tyr Lys Leu Asp Ile Glu Pro Ile Asp Asn Asp
 68 180 185 190
 70 Asn Thr Ser Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln
 71 195 200 205

ENTERED

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73 Ala Cys Pro Lys Ile Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
 74 210 215 220
 76 Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Ser Gly
 77 225 230 235 240
 79 Lys Gly Ser Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
 80 245 250 255
 82 Arg Pro Val Val Ser Thr Gln Leu Leu Asn Gly Ser Leu Ala Glu
 83 260 265 270
 85 Glu Glu Val Val Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr
 86 275 280 285
 88 Ile Ile Val Gln Leu Arg Glu Pro Val Lys Ile Asn Cys Ser Arg Pro
 89 290 295 300
 91 Asn Asn Asn Thr Arg Lys Ser Ile Pro Met Gly Pro Gly Arg Ala Phe
 92 305 310 315 320
 94 Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn
 95 325 330 335
 97 Ile Ser Lys Thr Asn Trp Thr Asn Ala Leu Lys Gln Val Val Glu Lys
 98 340 345 350
 100 Leu Gly Glu Gln Phe Asn Lys Thr Lys Ile Val Phe Thr Asn Ser Ser
 101 355 360 365
 103 Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Ala Gly Glu
 104 370 375 380
 106 Phe Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asp Ser Ile Trp Asn Ser
 107 385 390 395 400
 109 Glu Asn Gly Thr Trp Asn Ile Thr Arg Gly Leu Asn Asn Thr Gly Arg
 110 405 410 415
 112 Asn Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg
 113 420 425 430
 115 Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Lys Gly Asn
 116 435 440 445
 118 Ile Ser Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
 119 450 455 460
 121 Gly Lys Asp Asp Asn Ser Arg Asp Gly Asn Glu Thr Phe Arg Pro Gly
 122 465 470 475 480
 124 Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys
 125 485 490 495
 127 Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg
 128 500 505 510
 130 Arg Val Val Gln Arg Glu Glu Arg Ala Val Gly Leu Gly Ala Met Phe
 131 515 520 525
 133 Ile Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Val
 134 530 535 540
 136 Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln
 137 545 550 555 560
 139 Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln
 140 565 570 575
 142 Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val
 143 580 585 590
 145 Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser

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146	595	600	605
148	Gly Lys Leu Ile Cys Thr Thr Val Pro Trp Asn Ala Ser Trp Ser		
149	610	615	620
151	Lys Asn Lys Thr Leu Glu Ala Ile Trp Asn Asn Met Thr Trp Met Gln		
152	625	630	635
154	640	Trp Asp Lys Glu Ile Asp Asn Tyr Thr Lys Leu Ile Tyr Ser Leu Ile	
155	645	650	655
157	Glu Glu Ser Gln Ile Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu		
158	660	665	670
160	Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser Asn Trp		
161	675	680	685
163	Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly		
164	690	695	700
166	Leu Arg Ile Val Phe Val Val Leu Ser Ile Val Asn Arg Val Arg Gln		
167	705	710	715
169	720	Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Ala Pro Arg Gly	
170	725	730	735
172	Pro Asp Arg Pro Glu Glu Ile Glu Glu Gly Gly Asp Arg Asp Arg		
173	740	745	750
175	Asp Arg Ser Gly Leu Leu Val Asp Gly Phe Leu Thr Leu Ile Trp Val		
176	755	760	765
178	Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu		
179	770	775	780
181	Leu Leu Ile Val Thr Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp		
182	785	790	795
184	800	Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu	
185	805	810	815
187	Leu Lys Asn Ser Ala Val Ser Leu Phe Asn Ala Thr Ala Ile Ala Val		
188	820	825	830
190	Ala Glu Gly Thr Asp Arg Val Ile Glu Val Leu Gln Arg Val Gly Arg		
191	835	840	845
193	Ala Leu Leu His Ile Pro Thr Arg Ile Arg Gln Gly Leu Glu Arg Ala		
194	850	855	860
196	Leu Leu		
197	865		
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201	<211> LENGTH: 17		
202	<212> TYPE: PRT		
203	<213> ORGANISM: Human immunodeficiency virus type 1		
205	<220> FEATURE:		
206	<223> OTHER INFORMATION: segment of R2 strain V3 domain		
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216	<210> SEQ ID NO: 3		
217	<211> LENGTH: 35		
218	<212> TYPE: PRT		
219	<213> ORGANISM: Human immunodeficiency virus type 1		

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221 <220> FEATURE:
222 <223> OTHER INFORMATION: R2 strain V3 domain
224 <400> SEQUENCE: 3
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226 1 5 10 15
228 Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln
229 20 25 30
231 Ala His Cys
232 35
235 <210> SEQ ID NO: 4
236 <211> LENGTH: 35
237 <212> TYPE: PRT
238 <213> ORGANISM: Human immunodeficiency virus type 1
240 <220> FEATURE:
241 <223> OTHER INFORMATION: V3 domain of strain 93TH966.8
243 <400> SEQUENCE: 4
244 Cys Thr Arg Pro Ser Asn Asn Thr Arg Thr Ser Thr Thr Ile Gly Pro
245 1 5 10 15
247 Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr Gly Asn Ile Arg Lys
248 20 25 30
250 Ala Tyr Cys
251 35

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/762,261A

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TIME: 08:45:07

Input Set : A:\Hj500lus.app

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